PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/486,409*

AU 1804

DATE: 05/12/96
TIME: 11:38:53

INPUT SET: S10475.raw

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> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

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1                            SEQUENCE LISTING
2
3   (1)    General Information:
4
5        (i) APPLICANT: WAHL, DR., GEOFFREY M.
6                       O'GORMAN DR., STEPHEN V.
7
8       (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
9               MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
10              THEREFOR
11
12     (iii) NUMBER OF SEQUENCES: 4
13
14      (iv) CORRESPONDENCE ADDRESS:
15            (A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
16            (B) STREET: 444 South Flower Street, Suite 2000
17            (C) CITY: Los Angeles
18            (D) STATE: CA
19            (E) COUNTRY: USA
20            (F) ZIP: 90071
21
22       (v) COMPUTER READABLE FORM:
23            (A) MEDIUM TYPE: Floppy disk
24            (B) COMPUTER: IBM PC compatible
25            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26            (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28      (vi) CURRENT APPLICATION DATA:
29            (A) APPLICATION NUMBER: US 08/486,409
30            (B) FILING DATE: 07-JUN-1995
31            (C) CLASSIFICATION: 435
32
33     (vii) PRIOR APPLICATION DATA:
34            (A) APPLICATION NUMBER: US/08/147,912
35            (B) FILING DATE: 03-NOV-1993
36
37            (A) APPLICATION NUMBER: US 07/666,252
38            (B) FILING DATE: 08-MAR-1991
39
40    (viii) ATTORNEY/AGENT INFORMATION:
41            (A) NAME: REITER MR., STEPHEN E.
42            (B) REGISTRATION NUMBER: 31192
43            (C) REFERENCE/DOCKET NUMBER: P31 8929
44
45      (ix) TELECOMMUNICATION INFORMATION:
46            (A) TELEPHONE: (619) 535-9001
```

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47              (B) TELEFAX: (619) 535-8949
48
49
50   (2) INFORMATION FOR SEQ ID NO:1:
51
52       (i) SEQUENCE CHARACTERISTICS:
53           (A) LENGTH: 1380 base pairs
54           (B) TYPE: nucleic acid
55           (C) STRANDEDNESS: single
56           (D) TOPOLOGY: linear
57
58      (ii) MOLECULE TYPE: DNA (genomic)
59
60
61     (vii) IMMEDIATE SOURCE:
62           (B) CLONE: NATIVE FLP
63
64      (ix) FEATURE:
65           (A) NAME/KEY: CDS
66           (B) LOCATION: 1..1269
67
68
69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
70
71   ATG CCA CAA TTT GAT ATA TTA TGT AAA ACA CCA CCT AAG GTG CTT GTT        48
72   Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
73    1               5                  10                  15
74
75   CGT CAG TTT GTG GAA AGG TTT GAA AGA CCT TCA GGT GAG AAA ATA GCA        96
76   Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
77               20                  25                  30
78
79   TTA TGT GCT GCT GAA CTA ACC TAT TTA TGT TGG ATG ATT ACA CAT AAC       144
80   Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
81           35                  40                  45
82
83   GGA ACA GCA ATC AAG AGA GCC ACA TTC ATG AGC TAT AAT ACT ATC ATA       192
84   Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
85           50                  55                  60
86
87   AGC AAT TCG CTG AGT TTC GAT ATT GTC AAT AAA TCA CTC CAG TTT AAA       240
88   Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
89    65                  70                  75                  80
90
91   TAC AAG ACG CAA AAA GCA ACA ATT CTG GAA GCC TCA TTA AAG AAA TTG       288
92   Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
93                   85                  90                  95
94
95   ATT CCT GCT TGG GAA TTT ACA ATT ATT CCT TAC TAT GGA CAA AAA CAT       336
96   Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
97               100                 105                 110
98
99   CAA TCT GAT ATC ACT GAT ATT GTA AGT AGT TTG CAA TTA CAG TTC GAA       384
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100    Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
101        115             120             125
102

103    TCA TCG GAA GAA GCA GAT AAG GGA AAT AGC CAC AGT AAA AAA ATG CTT    432
104    Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
105        130             135             140
106

107    AAA GCA CTT CTA AGT GAG GGT GAA AGC ATC TGG GAG ATC ACT GAG AAA    480
108    Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
109    145             150             155             160
110

111    ATA CTA AAT TCG TTT GAG TAT ACT TCG AGA TTT ACA AAA ACA AAA ACT    528
112    Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
113                165             170             175
114

115    TTA TAC CAA TTC CTC TTC CTA GCT ACT TTC ATC AAT TGT GGA AGA TTC    576
116    Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
117                180             185             190
118

119    AGC GAT ATT AAG AAC GTT GAT CCG AAA TCA TTT AAA TTA GTC CAA AAT    624
120    Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
121                195             200             205
122

123    AAG TAT CTG GGA GTA ATA ATC CAG TGT TTA GTG ACA GAG ACA AAG ACA    672
124    Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
125        210             215             220
126

127    AGC GTT AGT AGG CAC ATA TAC TTC TTT AGC GCA AGG GGT AGG ATC GAT    720
128    Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
129    225             230             235             240
130

131    CCA CTT GTA TAT TTG GAT GAA TTT TTG AGG AAT TCT GAA CCA GTC CTA    768
132    Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
133                245             250             255
134

135    AAA CGA GTA AAT AGG ACC GGC AAT TCT TCA AGC AAT AAA CAG GAA TAC    816
136    Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
137                260             265             270
138

139    CAA TTA TTA AAA GAT AAC TTA GTC AGA TCG TAC AAT AAA GCT TTG AAG    864
140    Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
141        275             280             285
142

143    AAA AAT GCG CCT TAT TCA ATC TTT GCT ATA AAA AAT GGC CCA AAA TCT    912
144    Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
145        290             295             300
146

147    CAC ATT GGA AGA CAT TTG ATG ACC TCA TTT CTT TCA ATG AAG GGC CTA    960
148    His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
149    305             310             315             320
150

151    ACG GAG TTG ACT AAT GTT GTG GGA AAT TGG AGC GAT AAG CGT GCT TCT   1008
152    Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
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153                        325                  330                   335
154
155     GCC GTG GCC AGG ACA ACG TAT ACT CAT CAG ATA ACA GCA ATA CCT GAT        1056
156     Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
157                 340                  345                  350
158
159     CAC TAC TTC GCA CTA GTT TCT CGG TAC TAT GCA TAT GAT CCA ATA TCA        1104
160     His Tyr Phe Ala Leu Val Ser Arg Tyr Tyr Ala Tyr Asp Pro Ile Ser
161             355                  360                  365
162
163     AAG GAA ATG ATA GCA TTG AAG GAT GAG ACT AAT CCA ATT GAG GAG TGG        1152
164     Lys Glu Met Ile Ala Leu Lys Asp Glu Thr Asn Pro Ile Glu Glu Trp
165         370                  375                  380
166
167     CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC        1200
168     Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr
169     385                  390                  395                  400
170
171     CCC GCA TGG AAT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA        1248
172     Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser
173                 405                  410                  415
174
175     TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT           1299
176     Ser Tyr Ile Asn Arg Arg Ile
177                 420
178
179     ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA      1359
180
181     ACAGTGAGCT GTATGTGCGC A                                                1380
182
183
184     (2) INFORMATION FOR SEQ ID NO:2:
185
186             (i) SEQUENCE CHARACTERISTICS:
187                 (A) LENGTH: 423 amino acids
188                 (B) TYPE: amino acid
189                 (D) TOPOLOGY: linear
190
191         (ii) MOLECULE TYPE: protein
192
193         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
194
195     Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val
196      1               5                  10                  15
197
198     Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala
199                 20                  25                  30
200
201     Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn
202             35                  40                  45
203
204     Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile
205         50                  55                  60
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206
207    Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys
208     65              70              75                      80
209
210    Tyr Lys Thr Gln Lys Ala Thr Ile Leu Glu Ala Ser Leu Lys Lys Leu
211             85              90                      95
212
213    Ile Pro Ala Trp Glu Phe Thr Ile Ile Pro Tyr Tyr Gly Gln Lys His
214            100             105                     110
215
216    Gln Ser Asp Ile Thr Asp Ile Val Ser Ser Leu Gln Leu Gln Phe Glu
217            115             120                     125
218
219    Ser Ser Glu Glu Ala Asp Lys Gly Asn Ser His Ser Lys Lys Met Leu
220        130             135                 140
221
222    Lys Ala Leu Leu Ser Glu Gly Glu Ser Ile Trp Glu Ile Thr Glu Lys
223    145             150                 155                     160
224
225    Ile Leu Asn Ser Phe Glu Tyr Thr Ser Arg Phe Thr Lys Thr Lys Thr
226            165                 170                     175
227
228    Leu Tyr Gln Phe Leu Phe Leu Ala Thr Phe Ile Asn Cys Gly Arg Phe
229            180                 185                 190
230
231    Ser Asp Ile Lys Asn Val Asp Pro Lys Ser Phe Lys Leu Val Gln Asn
232            195                 200                 205
233
234    Lys Tyr Leu Gly Val Ile Ile Gln Cys Leu Val Thr Glu Thr Lys Thr
235        210             215                 220
236
237    Ser Val Ser Arg His Ile Tyr Phe Phe Ser Ala Arg Gly Arg Ile Asp
238    225             230                 235                     240
239
240    Pro Leu Val Tyr Leu Asp Glu Phe Leu Arg Asn Ser Glu Pro Val Leu
241            245                 250                     255
242
243    Lys Arg Val Asn Arg Thr Gly Asn Ser Ser Ser Asn Lys Gln Glu Tyr
244            260                 265                 270
245
246    Gln Leu Leu Lys Asp Asn Leu Val Arg Ser Tyr Asn Lys Ala Leu Lys
247        275                 280                 285
248
249    Lys Asn Ala Pro Tyr Ser Ile Phe Ala Ile Lys Asn Gly Pro Lys Ser
250        290                 295                 300
251
252    His Ile Gly Arg His Leu Met Thr Ser Phe Leu Ser Met Lys Gly Leu
253    305             310                 315                     320
254
255    Thr Glu Leu Thr Asn Val Val Gly Asn Trp Ser Asp Lys Arg Ala Ser
256            325                 330                     335
257
258    Ala Val Ala Arg Thr Thr Tyr Thr His Gln Ile Thr Ala Ile Pro Asp
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/486,409*

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